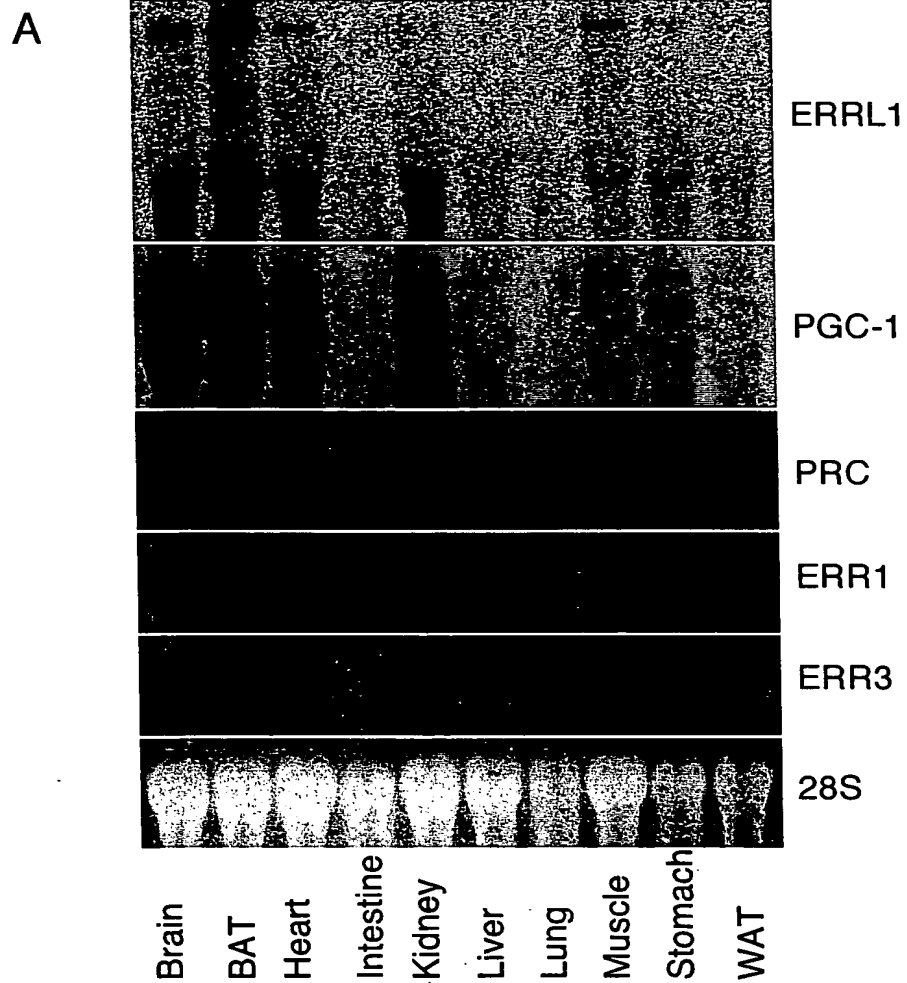


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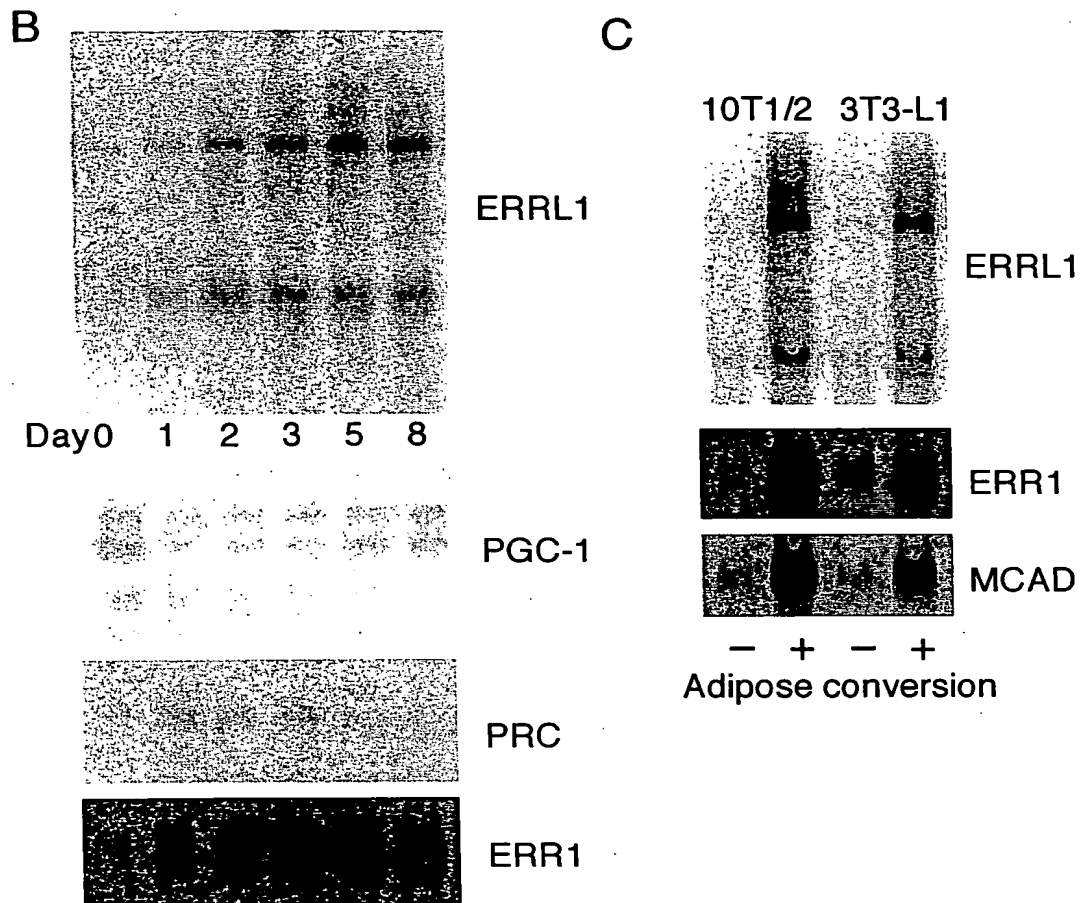
Fig. 1

ERRL1	MAGNDCGALLDEELSSFFLNYSLTQGGDSGEEQ-LCADLPELDLSQLDASDFDSATCFG	59
PGC-1	MAWDMCSQDSVWSIDIECAALVGEDQPLCPDLPELDLSELVDNDLDTDSFLG	51
	*** ** *	
ERRL1	ELQWCPETSETEPSQYSPDDSELFQ-IDSENEA-LLAALTKTLDDIPEDDVGLAAFPELD	117
PGC-1	GLKWCSDQSEIISNQYNNEPANIFEKIDEENEANLLAVLTETLDSLVPDEGLPSFDALT	111
	* ** ** *	
ERRL1	EGDTPSCTPASAPLSAPPSPTLERLLSPASDVDELSSLLQKLLLATSSPTASSDALKDGA	177
PGC-1	DGAVTTDNEASPSSM---PDGT-----PPPQEAEEPSLLKLLAPANTQLSYNECSGLS	163
	* *** * *	
ERRL1	TWSQTSLS---RSQRPCVKVDGTQDKKPTTL---RAQSRPCTELHKHLTSVLPCPRVK	230
PGC-1	TQNHAANHTRIRTNPAIVKTENSWSNKAASICQQQKPORRPECSELLKYLTINDDPHTK	223
	* * ** *	
ERRL1	ACSPTPHPSRLLSKEE-----EEEVGEDCPSPW---LTPASPQDSLAQDTASPDQAQPP	282
PGC-1	PTENRNSSRDKASKKKSHTQPQSQHAQAKPTTSLPLTPESPNDP-----KGSPFEN---	276
	** * *** *	
ERRL1	EEDVRAMVQLIRYMHTYCLPQRKLPQRAPEPIQACSSLSRQVQPRSRHPPKAFWTEFSI	342
PGC-1	-----	
ERRL1	LRELLAQDILCDVSKPYRLAIPVYASLTPQSRPRPPKDSQASPAHSAMAEVRITASPKS	402
PGC-1	-----	
ERRL1	TGPRPSLRPLRLEVKRDVNKPTRQKREDEEEEEEEEEEEEEEEEEEWGRKRPGRGLP	462
PGC-1	-----	
ERRL1	WTKLGRKMDSSVCPVRRSRRLNPELGPWLTFTEPLGALPSMCLDTETHNLEEDLGSLTD	522
PGC-1	-----	
ERRL1	SSQGRQLPQGSQIPALESPECSEGCSDTDEDPSCPQPTSRDSSRCLMLALSQSDSLGKXSF	582
PGC-1	-----KTI	279
	*	
ERRL1	EESLTVELCGTAGLTPPTTPPYKPMEDPFKPDTKLSPGQDTAPSLPSPEAL--PLTATP	640
PGC-1	ERTLSVELSGTAGLTPPTTPPHKANQDNPFKASPKLKPSCKTVVPPPTKRARYSECSGTQ	339
	* * *** ** *	
ERRL1	GASHKLPKRHPERSEILSHLQHAT--TQVVSQAGQKRPFCSCSFGDHDYCOVLREPAALQR	698
PGC-1	G-SHST-KKGPEQSEIYAQLSKSSGLSRGHEERKTKRPSLRFLGDHDYCOQLNSKTDILI	397
	* ** * ** *	
ERRL1	KV---LRSWEPIGVHLEDLAQQGAPLPTETKAP---RR--EANQNCDPHTKDSMQLRDHE	750
PGC-1	NISQELQDSRQLDFKDASCDWQGHICSSTDSGQCYLRETLEASKQVSPCSTRK-QLQDQE	456
	* ** ** *	
ERRL1	IRASLTKHFGLLETALEGEDLASCKSPEYDTVFEDSSSS-----SGES-SFLLEEEE	802
PGC-1	IRAEINKHFGHPCQAVF-DDKSDKTSELRDGDFSNEQFSKLPVFINSGLAMDGLFDDSED	515
	*** * ** *	
ERRL1	EEEGGEEDDEGEDS-----GVSPPCSD-HCPYQ---SPP---SKASRQLCSRSRSSSGSS	850
PGC-1	ESDKLSYPWDGTQPYSLFDVSPSCSSFNSPCRDSVSPPKSLFSQRPQMRSRSRSESRHR	575
	* * *** *	
ERRL1	SCS-----SWSPATRKN-----FRRESRGPCS-----DG	874
PGC-1	SCSRSPYSRSPSRSPGSRSSSRSCYSSHYRHRTHRNSPLYVRSRSPYSRRPRYDS	635
	*** * ** *	
ERRL1	TPSVRHAR-----KRRE---KAIGEGRVVYIRNLSSDMSSRELKKR	912
PGC-1	YEAYEHERLKRDEYRKEHEKRESERAKQEROKQKAEERRVYVVGKIRPDTTRTELDR	695
	* * * ** *	
ERRL1	FEVFGEIVECQVLT	970
PGC-1	FEVFGEIEECTVNL	752
	***** ** *	
ERRL1	RHFRWPRYTDYDPTSEESLPSSGKSKYEAMDFDLSLLKEAQQSLH	1014
PGC-1	KQFFKSNYADLDTNSDDFDPASTKSKYDSLDFDLSLLKEAQRSLRR	797
	* * * * *	

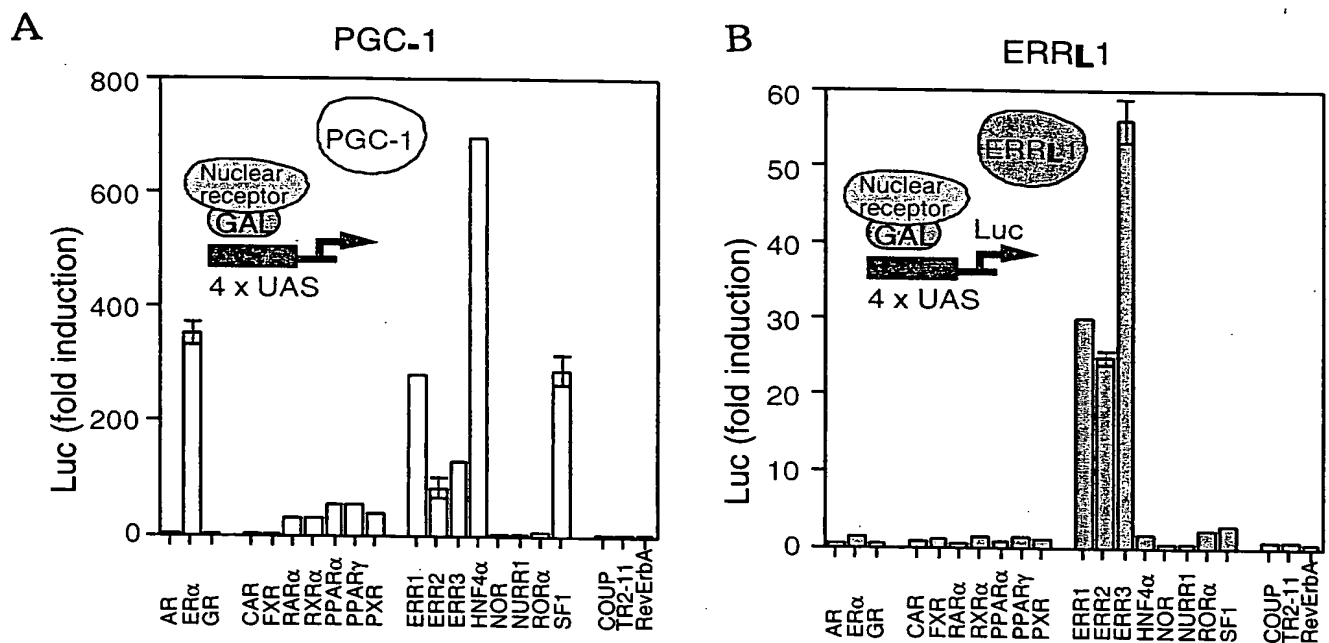
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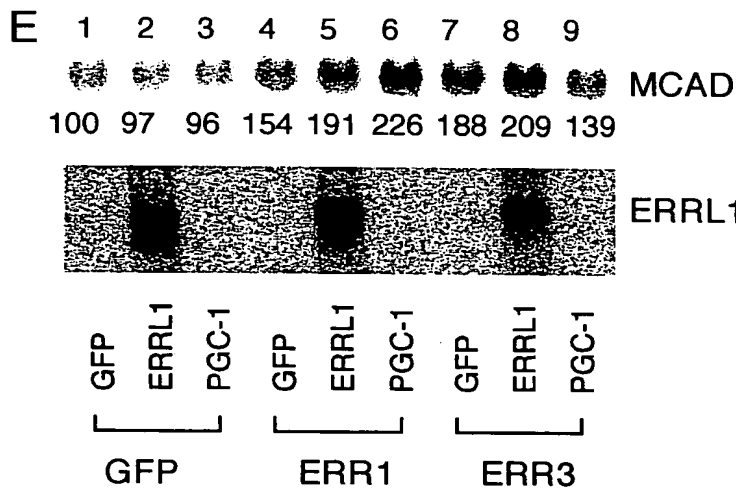


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Fig. 3

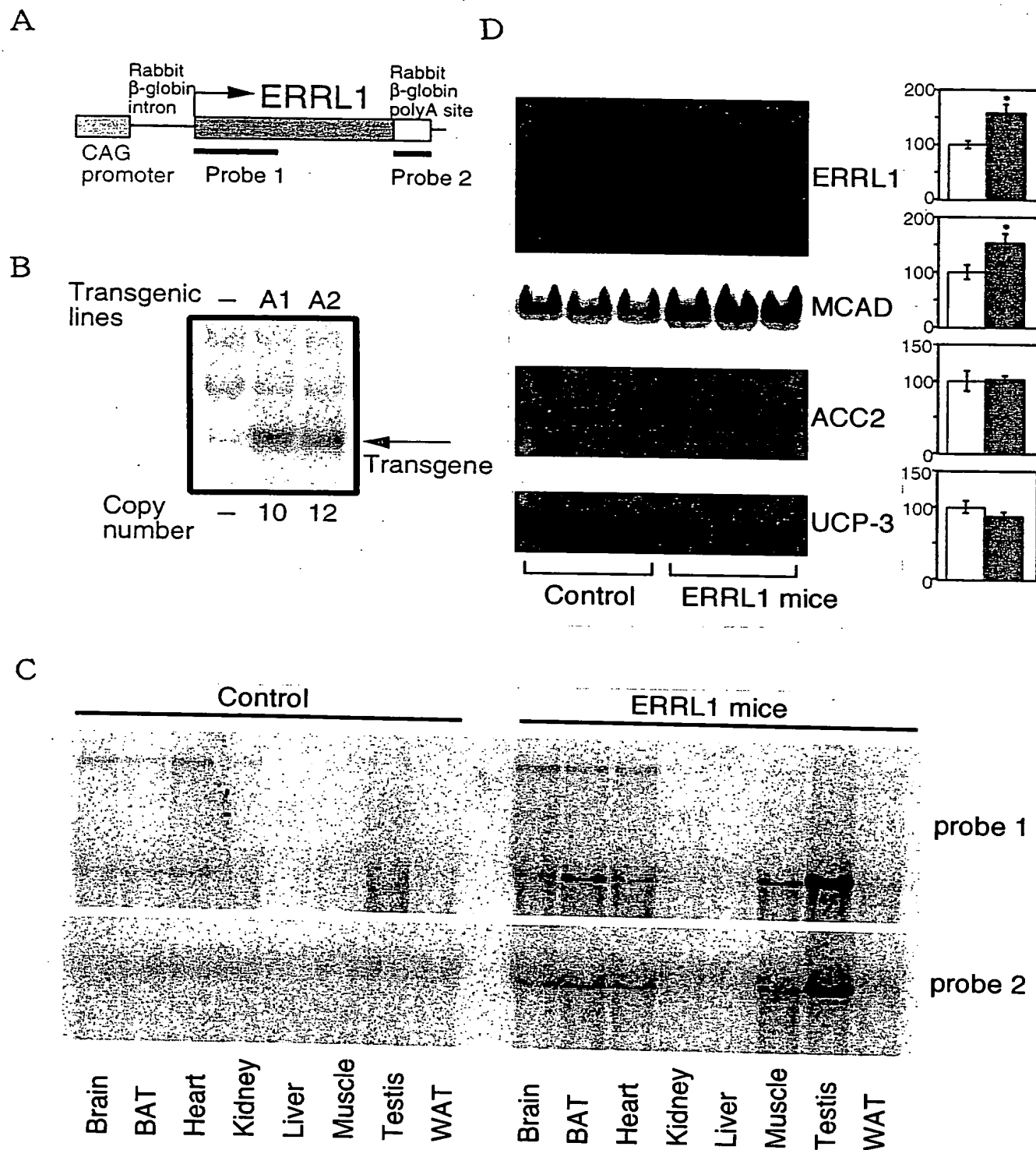


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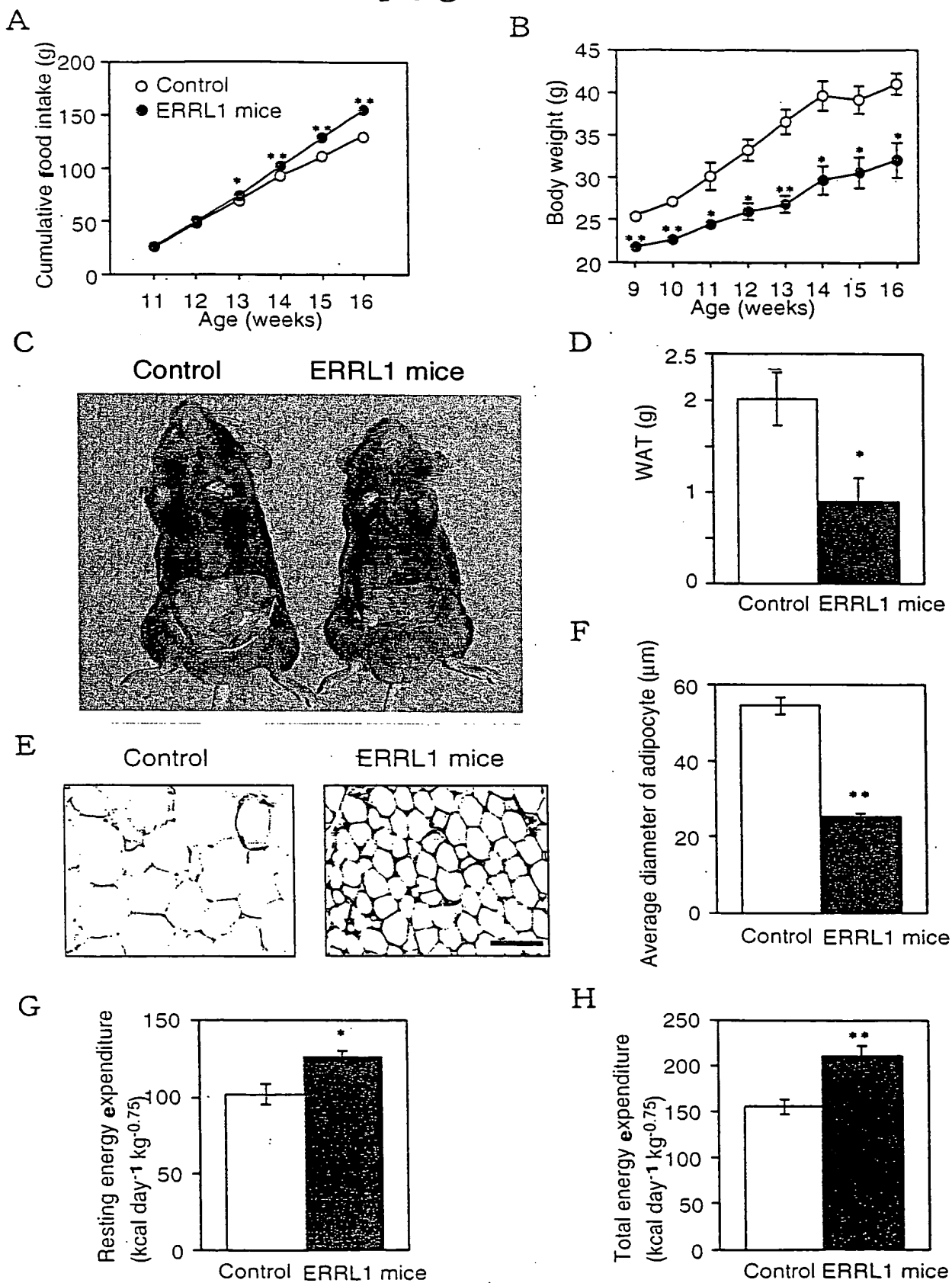


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Fig. 4



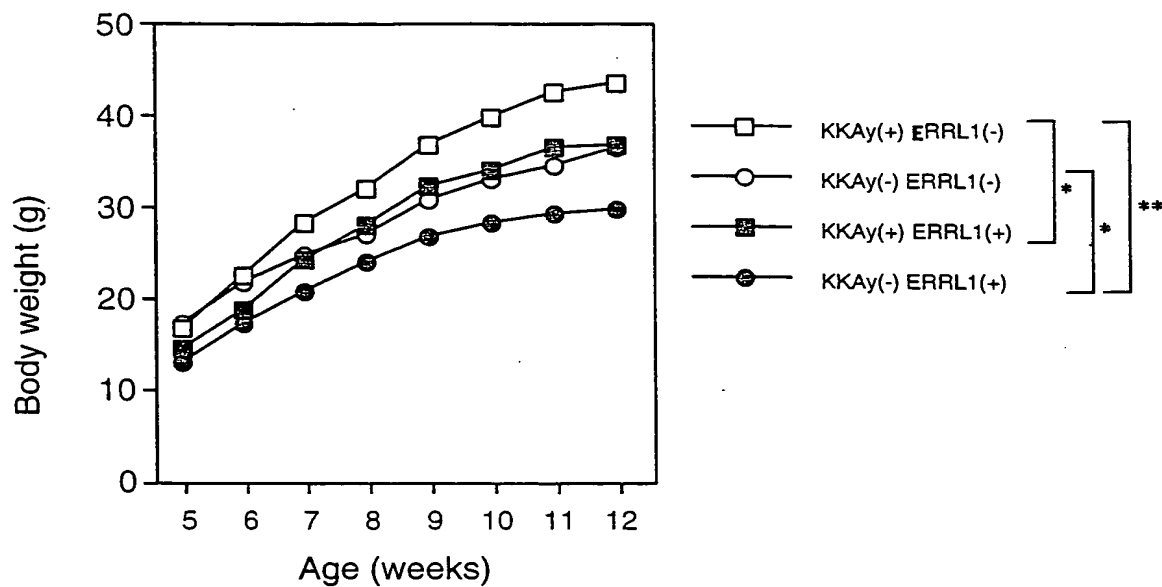
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Fig. 5



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Fig. 6

A



B

